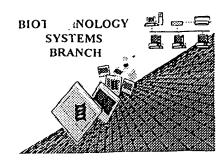*U   Uorriman*

RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: *09/509,449*

Source: *1648*

Date Processed by STIC: *2-22-01*

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RAW SEQUENCE LISTING   DATE: 02/22/2001
PATENT APPLICATION: US/09/509,449   TIME: 12:05:50

Input Set : A:\ST25.txt
Output Set: N:\CRF3\02222001\I509449.raw

```
 3 <110> APPLICANT: Aoyagi, Katsumi
 4         Ohue, Chiharu
 5         Iida, Kumiko
 6         Yagi, Shintaro
 8 <120> TITLE OF INVENTION: Method for Measurement of Hepatitis C Virus
10 <130> FILE REFERENCE: 594.352USWO
12 <140> CURRENT APPLICATION NUMBER: 09/509,449
13 <141> CURRENT FILING DATE: 2000-03-28
15 <150> PRIOR APPLICATION NUMBER: JP-10-216094
16 <151> PRIOR FILING DATE: 1998-07-30
18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04129
19 <151> PRIOR FILING DATE: 1999-07-30
21 <160> NUMBER OF SEQ ID NOS: 12
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 177
27 <212> TYPE: PRT
28 <213> ORGANISM: Hepatitis C virus
30 <400> SEQUENCE: 1
32 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Pro Glu
33 1               5                   10                  15
35 Phe Met Gly Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr
36             20                  25                  30
38 Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val
39         35                  40                  45
41 Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg
42     50                  55                  60
44 Ala Thr Arg Lys Thr Ser Lys Arg Ser Gln Pro Arg Gly Gly Arg Arg
45 65                  70                  75                  80
47 Pro Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro
48                 85                  90                  95
50 Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly
51             100                 105                 110
53 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp
54             115                 120                 125
56 Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr
57     130                 135                 140
59 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Phe Arg Val Gly Ala Phe
60 145                 150                 155                 160
62 Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu
63                 165                 170                 175
65 Asp
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 160
70 <212> TYPE: PRT
71 <213> ORGANISM: Hepatitis C virus
73 <400> SEQUENCE: 2
```

```
75  Met Gly Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
76  1               5                   10                  15
78  Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
79              20                  25                  30
81  Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
82              35                  40                  45
84  Thr Arg Lys Thr Ser Lys Arg Ser Gln Pro Arg Gly Gly Arg Arg Pro
85          50                  55                  60
87  Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly
88  65                  70                  75                  80
90  Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
91                  85                  90                  95
93  Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
94                  100                 105                 110
96  Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr Cys
97          115                 120                 125
99  Gly Phe Ala Asp Leu Met Gly Tyr Ile Phe Arg Val Gly Ala Phe Leu
100         130                 135                 140
102 Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
103 145                 150                 155                 160
105 <210> SEQ ID NO: 3
106 <211> LENGTH: 20
107 <212> TYPE: PRT
108 <213> ORGANISM: Artificial
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
113 <400> SEQUENCE: 3
115 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
116 1               5                   10                  15
118 Leu Pro Arg Arg
119         20
121 <210> SEQ ID NO: 4
122 <211> LENGTH: 10
123 <212> TYPE: PRT
124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
129 <400> SEQUENCE: 4
131 Gly Pro Arg Leu Gly Val Arg Ala Thr Arg
132 1               5                   10
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 21
136 <212> TYPE: PRT
137 <213> ORGANISM: Artificial
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
142 <400> SEQUENCE: 5
144 Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg His Arg
145 1               5                   10                  15
```

RAW SEQUENCE LISTING   DATE: 02/22/2001
PATENT APPLICATION: US/09/509,449   TIME: 12:05:50

Input Set : A:\ST25.txt
Output Set: N:\CRF3\02222001\I509449.raw

```
147 Ser Arg Asn Val Gly
148             20
150 <210> SEQ ID NO: 6
151 <211> LENGTH: 20 .
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
158 <400> SEQUENCE: 6
160 Asp Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
161 1             5                   10                  15
163 Thr Cys Gly Phe
164             20
166 <210> SEQ ID NO: 7
167 <211> LENGTH: 24
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Primer for polymerase chain reaction.
174 <400> SEQUENCE: 7
175 gaattcatgg gcacgaatcc taaa                                    24
178 <210> SEQ ID NO: 8
179 <211> LENGTH: 21
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Primer for polymerase chain reaction.
186 <400> SEQUENCE: 8
187 ttagtcctcc agaacccgga c                                       21
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 16
192 <212> TYPE: PRT
193 <213> ORGANISM: Artificial
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Portion of Hepatitis C virus sequence.
198 <400> SEQUENCE: 9
200 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile
201 1             5                   10                  15
203 <210> SEQ ID NO: 10
204 <211> LENGTH: 1197
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Nucleotide sequence coding for chimeric antigen.
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (1)..(1188)
215 <400> SEQUENCE: 10
216 gaa ttc acc aaa gtg ccg gtt gct tat gcg gcc aaa ggt tat aag gtc     48
```

RAW SEQUENCE LISTING   DATE: 02/22/2001
PATENT APPLICATION: US/09/509,449   TIME: 12:05:50

Input Set : A:\ST25.txt
Output Set: N:\CRF3\02222001\I509449.raw

```
217 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
218 1               5               10              15
220 ctg gtt ctg gac ccg agc gtt gcc agc acc ctg ggt ttc ggc gcg tat       96
221 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
222             20              25              30
224 ctg agc aag gcc cat ggt gtg aac ccg aac atc cgc acg ggc atc cgt      144
225 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
226         35              40              45
228 acc gtt acc acc ggt gct ccg gtg acc tat tcc acc tac ggt aaa tac      192
229 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
230     50              55              60
232 ctg gcg gac ggc ggt tgc gcc ggc ggt gcg tac gat gtg atc gga tct      240
233 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
234 65              70              75              80
236 gga gag gag gtg gcc ctg tct aac act gga gag gtc ccc ttc tat ggc      288
237 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
238             85              90              95
240 cgc gcg atc ccg atc gaa gcg atc aaa ggc ggt cgc cat ctg gtt ttc      336
241 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
242             100             105             110
244 tgc cat agc aag gag aaa tgc gat gaa ctg gcg agc gcg ctg tcc gga      384
245 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
246     115             120             125
248 ttg ggt ctg aac gct gtg gca ttc tat cgc ggt ctg gac gtg agc att      432
249 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser Ile
250     130             135             140
252 atc ccg acc cag ggc gat gtg gtt atc gtt agc acc gat gcg ctg atg      480
253 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met
254 145             150             155             160
256 acc ggt ttt acc ggc gat ttt gac tca gtg gtc gac tgt aac aca tgc      528
257 Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Val Asp Cys Asn Thr Cys
258             165             170             175
260 atc acc cag gga tct gga ctg gta agc ttc gcg agc cat gtg ccg tac      576
261 Ile Thr Gln Gly Ser Gly Leu Val Ser Phe Ala Ser His Val Pro Tyr
262             180             185             190
264 atc gag cag ggt atg caa ctg agc gaa caa ttt aag cag aag agc ctg      624
265 Ile Glu Gln Gly Met Gln Leu Ser Glu Gln Phe Lys Gln Lys Ser Leu
266             195             200             205
268 ggt ctg ctg cag acc gcg acc aaa cag gcg gag gcg gcc gcc ccg gtg      672
269 Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Pro Val
270     210             215             220
272 gtt ggc acc ccg aaa agc cgc cgt ccg gaa ggt cgt gcc tgg gcg caa      720
273 Val Gly Thr Pro Lys Ser Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln
274 225             230             235             240
276 ccg ggt acc atc atc ctg agc ggt cgt ccg gcg gtt gta ccg gat cgt      768
277 Pro Gly Thr Ile Ile Leu Ser Gly Arg Pro Ala Val Val Pro Asp Arg
278             245             250             255
280 gaa gtg ctg tat caa gaa ttt ctc gag gcc tct aga gcg gct ctc att      816
281 Glu Val Leu Tyr Gln Glu Phe Leu Glu Ala Ser Arg Ala Ala Leu Ile
```

```
282                  260                  265                  270
284 gaa gag ggg caa cgg ata gcc gag atg ctg aag tcc aag atc cag ggc        864
285 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly
286         275                  280                  285
288 tta ctg cag caa gcc tcc aag cag gcc caa gac ata aaa atc gac ggt        912
289 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly
290         290                  295                  300
292 acc ctg att att ccg aaa gat cgt cgc agc acc ggt aaa agc tgg ggt        960
293 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly
294 305                  310                  315                  320
296 aaa ccg ggc ttc ctc atc gat agc ttg cat atc aac cag cga gcc gtc       1008
297 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val
298         325                  330                  335
300 gtt gca ccg gac aag gag gtc ctt tat gag gct ttt gat gag atg gag       1056
301 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu
302         340                  345                  350
304 ctc gcc atg ggc acc aac ccg aaa ccg gag cgt aaa agc aag cgt aac       1104
305 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn
306         355                  360                  365
308 acc aac cgt aaa ccg cag gat att aaa ttc ccg ggt agt ggt cag gtg       1152
309 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val
310         370                  375                  380
312 gtg ggt ggt gtg tac ctg gtg ccg cgt cgt ggt ccg taaggatcc            1197
313 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro
314 385                  390                  395
317 <210> SEQ ID NO: 11
318 <211> LENGTH: 396
319 <212> TYPE: PRT
320 <213> ORGANISM: Artificial
322 <400> SEQUENCE: 11
324 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
325 1               5                   10                  15
328 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
329             20                  25                  30
332 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
333         35                  40                  45
336 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
337     50                  55                  60
340 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
341 65                  70                  75                  80
344 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
345             85                  90                  95
348 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
349             100                 105                 110
352 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
353         115                 120                 125
356 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser Ile
357     130                 135                 140
360 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met
```

(handwritten annotation with arrow from line 320) Missing mandatory <220>, <223> features to explain the source of the artificial sequence.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/509,449

DATE: 02/22/2001
TIME: 12:05:51

Input Set : A:\ST25.txt
Output Set: N:\CRF3\02222001\I509449.raw